SUPPLEMENTARY MATERIAL

Deaminase-independent inhibition of HIV-1 reverse transcription by APOBEC3G

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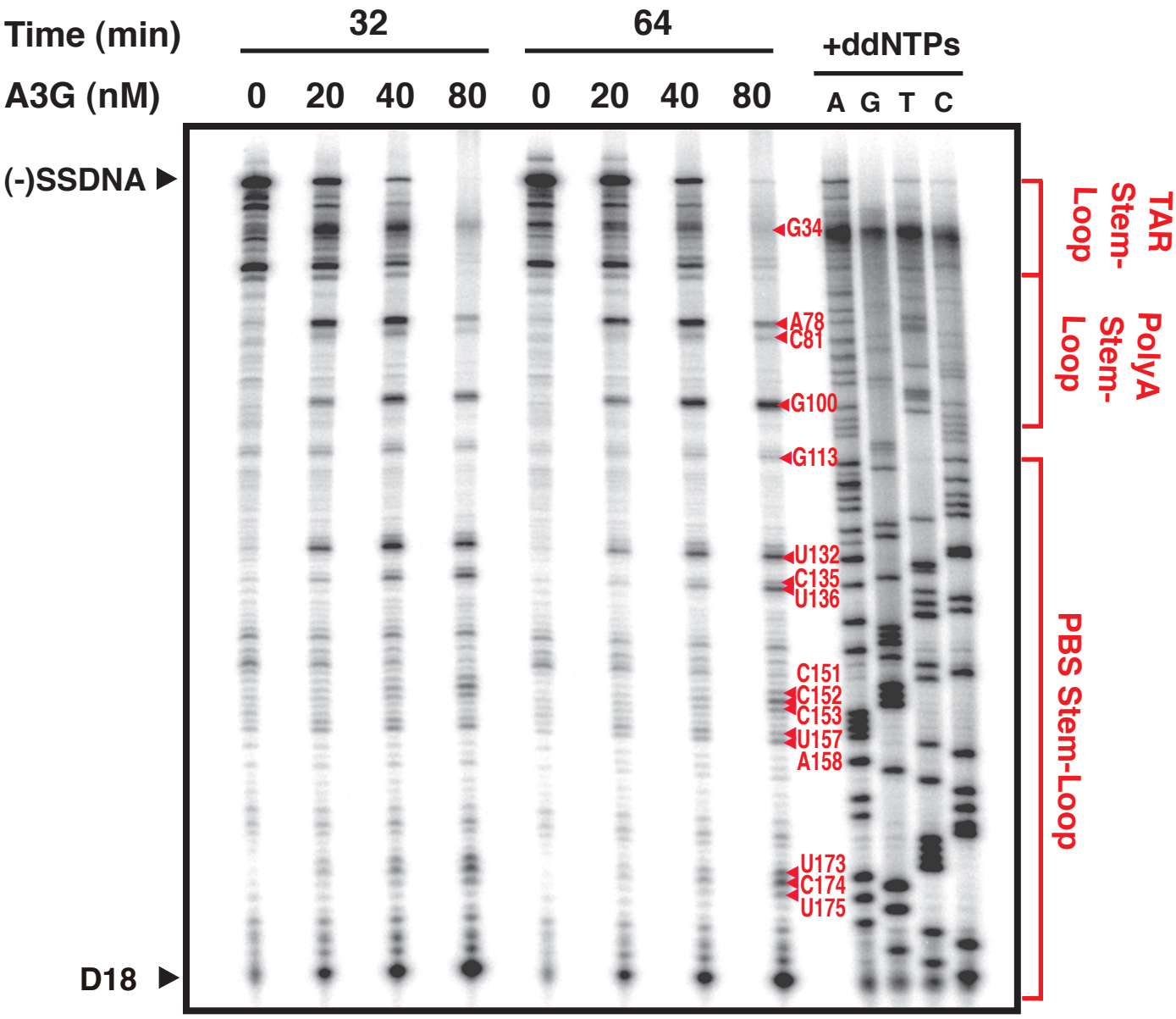
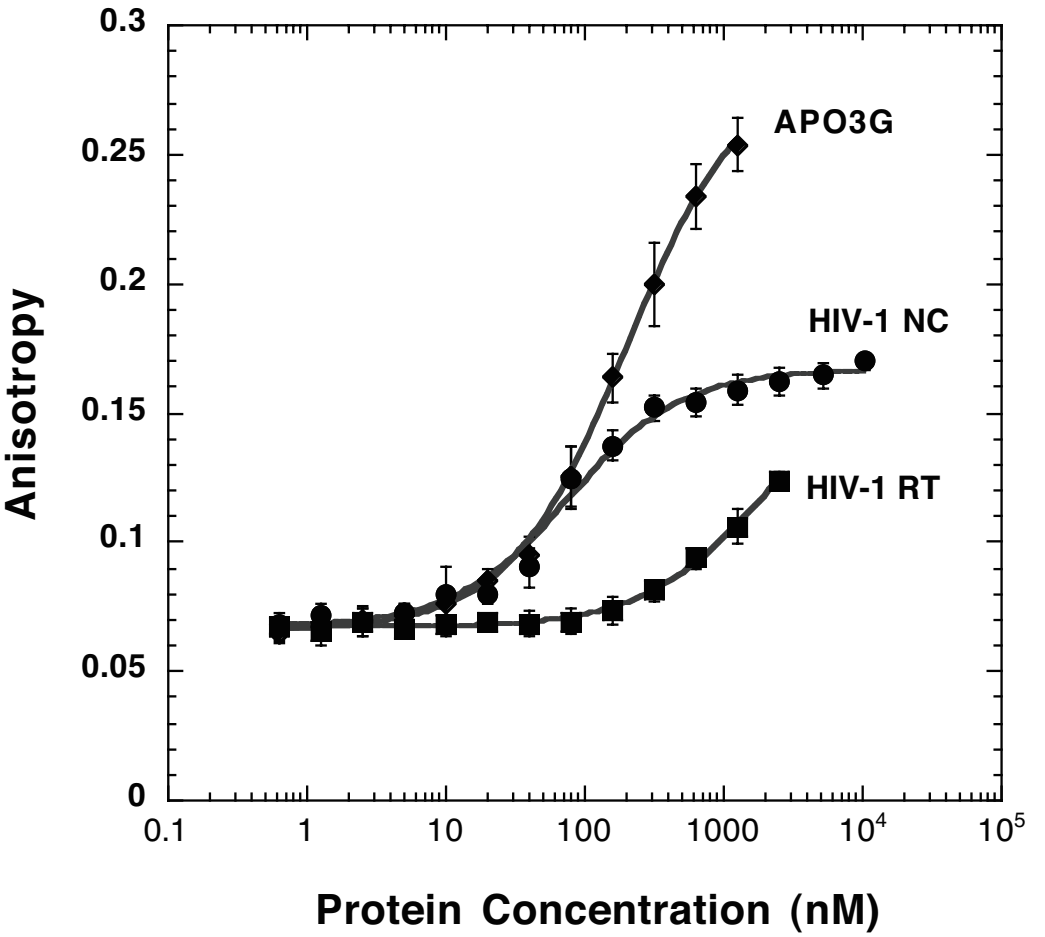
Figure S1


Time (min)
32
64
+ddNTPs
A3G (nM)
0 20 40 80 0 20 40 80
A G T C
(-)SSDNA
D18
G34
A78
C81
G100
G113
U132
C135
U136
C151
C152
C153
U157
A158
U173
C174
U175
TAR Stem-Loop
PolyA Stem-Loop
PBS Stem-Loop

Legend for Supplementary Figure S1

Figure S1. Effect of increasing concentrations of A3G on (-) SSDNA synthesis primed by D18. Data are shown for reactions incubated at 32 or 64 min in the absence of A3G or in the presence of 20, 40, or 80 nM A3G. Arrows point to the positions of the (-) SSDNA product and the D18 primer. Pause sites present only in reaction mixtures containing A3G (red arrows) were mapped on the RNA 244 template (bracketed headings highlighted in red) with the help of a sequencing ladder, shown on the right. Each sequencing reaction contained only one ddNTP. The residues where the A3G-specific RT pauses are found are labeled (to the right of the gel bands). These data were used to generate the diagram that appears in Figure 3C.

Figure S2


0.3
0.25
0.2
0.15
0.1
0.05
0
Anisotropy
APO3G
HIV-1 NC
HIV-1 RT
0.1
1
10
100
1000
10^4
10^5
Protein Concentration (nM)

Legend for Supplementary Figure S2

Figure S2. FA binding analysis. Various concentrations of HIV-1 NC, HIV-1 RT, or A3G were incubated with the 20-mer ssDNA, 5'-FAM-CTTCTTTGGGAGTGAATTAG-3' (JL587D). Anisotropy was plotted as a function of protein concentration in nM.